【Grant-in-Aid for Scientific Research(S)】
Biological Sciences (Biology)

Title of Project : Characterization of repetitive sequences by epigenetic and epigenomic approache

Tetsuji Kakutani
(National Institute of Genetics,
Department of Integrated Genetics, Professor)

Research Area : Genetics, genome dynamics

Keyword : transposon, DNA methylation, chromatin, evolution

【Purpose and Background of the Research】

Epigenetic regulation is involved in diverse biological phenomena, such as development, aging, and cancer. The progress of epigenetics in the last decade is partly due to the power of molecular genetics using model organisms. In addition, "epigenomic" approaches to examine DNA methylation and other chromatin modifications have accelerated the progress of this research field.

On the other hand, recent results by multiple groups have implicated that epigenetic control is important for chromosome behavior and genome evolution. Repetitive sequences are not only potential threat to the genome stability but also involved in more complex biological phenomena such as genomic imprinting, reproduction, and development. Here, through molecular genetics and genomics of Arabidopsis, we will investigate the mechanisms to confine DNA methylation in repetitive sequences and the dynamics of repetitive sequences at the genome-wide level.

【Research Methods】

(1) Characterization of transposon behavior at genome-wide level. Using genomic tilling array, we will examine modification and proliferation of transposons after external stimuli such as chromosome breaks and dedifferentiation. In addition, using mutants affecting epigenetic state, we will dissect the molecular mechanisms of the effects on the transposons. Furthermore, using natural strains of *A. thaliana* and other species in the genera *Arabidopsis*, we will try to understand the behavior of these transposons in the context of epigenetic controls.

(2) Mechanisms to exclude DNA methylation from genic regions. DNA methylation contributes to stabilization of genome through silencing of transposons. On the other hand, DNA methylation is excluded from active genes, which depends on a jmjC-domain containing protein IBM1. We will study the mechanisms that IBM1 distinguishes genes and transposons through genetic and genomic approaches.

【Expected Research Achievements and Scientific Significance】

We aim to understand transposon dynamics and genome evolution in the context of epigenetic controls. We also try to understand how the differential DNA methylation patterns between transposon and active genes are generated.

【Publications Relevant to the Project】

1. Tsukahara S, Kobayashi A, Kawabe A, Mathieu O, Miura A, and Kakutani T (2009) Bursts of retrotransposition reproduced in Arabidopsis. ***Nature*** 303, 423-426
2. Miura A, Nakmura M, Inagaki S, Kobayashi A, Saze H, and Kakutani T (2009) An Arabidopsis jmjC domain protein protects transcribed genes from DNA methylation at CHG sites. ***EMBO J.*** 28, 1078-1086
3. Saze H, Shiraishi A, Miura A, and Kakutani T (2008) Control of Genic DNA methylation by a jmjC domain-containing protein in Arabidopsis thaliana. ***Science*** 319, 462-465

【Term of Project】 FY2010-2014

【Budget Allocation】 106, 700 Thousand Yen

【Homepage Address and Other Contact Information】

http://www.nig.ac.jp/labs/AgrGen/home-j.html